REMARKS

INTRODUCTION:

In accordance with the foregoing, claims 16, 23 and 24 have been amended. No new matter is being presented, and approval and entry are respectfully requested.

Claims 16, 17, 23, 24, and 25 are under consideration. Claim 26 is withdrawn. Reconsideration is respectfully requested.

FURTHER REMARKS IN VIEW OF EXAMINER'S COMMENTS IN ADVISORY ACTION:

The Examiner submits: "The result provided by the determination of the instantly recited root mean square deviation performed on a given plurality of point sets dos not result in a distance, per se." (emphasis added) Applicants respectfully disagree. At http://en.wikipedia.org/wiki/Root_mean _square_deviation_ (bioinformatics), dated February 6, 2007, a copy of which is provided in the simultaneously filed Information Disclosure Statement, it recites:

> Root mean square deviation (bioinformatics)
>
> **From Wikipedia, the free encyclopedia**
> Jump to: navigation, search
>
> **root mean square deviation** (RMSD) is the measure of the average distance between the backbones of superimposed proteins. In the study of globular protein conformations, one customarily measures the similarity in three-dimensional structure by the RMSD of the Cα atomic coordinates after optimal rigid body superposition.
>
> A widely used way to compare the structures of biomolecules or solid bodies is to translate and rotate one structure with respect to the other to minimize the RMSD. Coutsias, *et al.* presented a simple derivation, based on quaternions, for the optimal solid body transformation (rotation-translation) that minimizes the RMSD between two sets of vectors.[1] They proved that the quaternion method is equivalent to the well-known formula due to Kabsch.[2]

Contents

[hide]

[edit] The equation

$$RMSD = \sqrt{\frac{1}{N}\sum_{i=1}^{i=N}\delta_i^2}$$

where δ is the distance between N pairs of equivalent atoms (usually $C\alpha$ and sometimes $C, N, O, C\beta$).

Normally a rigid superposition which minimizes the RMSD is performed, and this minimum is returned. Given two sets of n points $\mathbf{v}$and $\mathbf{w}$, the RMSD is defined as follows:

$$\mathrm{RMSD}(\mathbf{v}, \mathbf{w}) = \sqrt{\frac{1}{n}\sum_{i=1}^{n}\|v_i - w_i\|^2}$$

$$= \sqrt{\frac{1}{n}\sum_{i=1}^{n}(v_{ix} - w_{ix})^2 + (v_{iy} - w_{iy})^2 + (v_{iz} - w_{iz})^2}$$

An RMSD value is expressed in length units. The most commonly used unit in structural biology is the Ångström (Å) which is equal to 10^{-10}m."

Hence, it is clear that it is known to those skilled in the art that, in biometrics, a root mean square deviation (RMSD) is the measure of the average distance and an RMSD value is expressed in length units, as is done in the present application. Hence, Applicants respectfully submit that the result provided by the determination of the instantly recited root mean square deviation value performed on a given plurality of point sets does result in a distance value per se.

The Examiner refers to page 6, lines 8-11, of the Office Action mailed 11/22/2006, wherein the Examiner submitted: "These steps are initially unclear because it cannot be ascertained what kind of attributes can be associated to a first or second point set, as the claims fail to specify what information is encompassed by either a first or second point set." Claim 16, as amended, for example, recites in part:

> ... each of the plurality of probe subsets being expressed by three-dimensional coordinates of elements of secondary structures of probe structures, wherein a first subset of the plurality of probe subsets comprises a first point set of an amino acid sequence database or a motif database and each of the plurality of target subsets is expressed by three-dimensional coordinates of elements of the plurality of target subsets of secondary structures of a target structure, wherein a first subset of the plurality of target subsets comprises a second point set of an input amino acid sequence of the target structure, wherein each point of the first point set and the second point set is expressed by three-dimensional coordinates and the coordinates are analyzed to determine correspondence... (emphasis added)

As noted above in Wikipedia, it is known to those skilled in the art that "one customarily measures the similarity in three-dimensional structure by the RMSD of the Cα atomic coordinates after optimal rigid body superposition" (emphasis added). Hence, it is respectfully submitted that it is clear what information is encompassed by either a first or second point set. The remarks below explain what an attribute is.

With respect to the limitation "successively giving correspondence to an element constituting the set," the specification in paragraph [0014] states:

> [0014] When the researcher searches the similar three-dimensional, structure, an r.m.s.d. (root mean square distance) value is used as a scale of the similarity of the three-dimensional structures of the substances. The r.m.s.d. value is a value expressing a square root of a mean square distance between the corresponding elements constituting the substances. Empirically, the substances are thought to be exceedingly similar to each other in the case where the r.m.s.d value between the substances is not greater than 1 Å.

Hence, the terminology "successively giving correspondence to an element constituting the sets" clearly indicates that an element constituting the target set is determined to correspond to an element of a probe set, as indicated by paragraphs [0171] and [0172] of the specification:

> [0171] The substances A and B are expressed, respectively, by the point sets $A=\{a_1, a_2, \ldots, a_i, \ldots, a_m\}$, $1 \le i \le m$, and the point set $B=\{b_1, b_2, \ldots, b_j, \ldots, b_n\}$, $1 \le j \le n$. The respective points $a_i=(x_i, y_i, z_i)$ and $b_i=(x_j, y_j, z_j)$ are expressed as a three-dimensional coordinate. In the point set A, an order relationship is established: $a_1<a_2< \ldots <a_i< \ldots <a_m$ (or $a_1>a_2> \ldots >a_i> \ldots >a_m$). Likewise, in the point set B an order relationship is established: $b_1<b_2< \ldots <b_i< \ldots <b_n$ (or $b_1>b_2> \ldots >b_j> \ldots >b_n$).
>
> [0172] In this case, elements of these point sets are in principle related to each other in accordance with the order relationship, and all combinations can be generated by creating a tree structure shown in FIG. 16A. FIG. 16B shows an example case where the

point set A includes three elements and the point set B includes four elements. In other words, FIG. 16B shows the correspondence between the ordered point set A={a_1, a_2, a_3} (order relationship thereof is: $a_1<a_2<a_3$) and the ordered point set B={b_1, b_2, b_3, b_4} (order relationship thereof: $b_1<b_2<b_3<b_4$). (emphasis added)

Thus, it is respectfully submitted that the amendments do indeed clarify the issues set forth in the previous Office Action.

The Examiner submited that the terminology "pruning" was unclear. It is respectfully submitted that various examples of "pruning" are set forth in paragraphs [0198]-[0207] the specification:

[0197] (5) Refining of Candidates Based on a Threshold Value Condition

[0198] The point sets can be more efficiently related by setting a specified threshold value in the aforementioned methods (1) to (4), and pruning a retrieval path if an attribute value of a candidate is greater than this threshold value. As this threshold value, for example, restriction in a nil number (the number of nil) and restriction in a r.m.s.d. value can be used.

[0199] (a) Restriction in a Nil Number

[0200] When a total number of nil becomes too large among the generated combinations, meaningless candidates for combinations are generated as a result. Accordingly, in relating the elements of the point sets A and B, if the total number of nil becomes in excess of a given threshold value, the generation of the unnecessary candidates can be prevented by excluding these from the candidates, thereby relating the elements more efficiently.

[0201] FIG. 21 shows an example of pruning in a case where a total number of nil is restricted to 0 in relating a point set A={a.sub.1, a.sub.2, a.sub.3} to a point set B={b.sub.1, b.sub.2, b.sub.3, b.sub.4}. In this figure, a portion designated at x in a tree structure is a portion to be pruned.

[0202] (b) Restriction in an r.m.s.d. Value

[0203] In the case where an r.m.s.d. value of all the points related thus far becomes exceedingly bad by relating an element a_i of a point set A to an element b_i of a point set B, it is preferable to exclude this point from consideration of the candidates. In view of this, the r.m.s.d. value of all the points when the element a_i is related to the element b_i is calculated, and this point is selected as a candidate if the calculated r.m.s.d value is not greater than a given threshold value. On the contrary, this point is excluded from the candidates if the r.m.s.d value is in excess of the given threshold value. In this way, the candidates for a point to be related can be generated more efficiently.

[0204] (6) Refining of Candidates Based on an Attribute of a Point

[0205] The number of candidates for a point to be related can be reduced by using an attribute of the point in relating an element a_i of a point set A to an element b_i of a point set B. The attributes of the point, for example, include the type of an atom, an atomic

group, and a molecule, the hydrophilic property, the hydrophobic property, and the positive or negative charge. It is determined whether the point is selected as a candidate by checking whether these attributes coincide.

[0206] For example, in the case of relating elements constituting proteins, the number of candidates for a point to be related can be reduced by using the type of an amino acid residue (corresponding to an atomic group) as an attribute of the point. Regarding the types of amino acid residues or the like, please refer to references such as "Fundamental to Biochemistry," pp. 21-26, Tokyo Kagaku Dohjin Shuppan.

[0207] Further, the candidates for the point to be related can be reduced by adding a restriction to a specific element. For example, the candidates to be retrieved can be reduced by providing the restriction that the nil is not inserted to a certain point or by designating an attribute of point to a certain point.

With respect to the Examiner's concerns about the terminology "pruning," it is respectfully submitted that MPEP 2111 recites:

> The Patent and Trademark Office ("PTO") determines the scope of claims in patent applications not solely on the basis of the claim language, but upon giving claims their broadest reasonable construction "in light of the specification as it would be interpreted by one of ordinary skill in the art." *In re Am. Acad. of Sci. Tech. Ctr.*, 367 F.3d 1359, 1364[, 70 USPQ2d 1827] (Fed. Cir. 2004). Indeed, the rules of the PTO require that application claims must "conform to the invention as set forth in the remainder of the specification and the terms and phrases used in the claims must find clear support or antecedent basis in the description so that the meaning of the terms in the claims may be ascertainable by reference to the description." 37 CFR 1.75(d)(1). (emphasis added)

Hence, it is respectfully submitted that the terminology "pruning" is known to those skilled in the art and that examples of pruning are set forth in the specification. Thus, the scope and meaning of the terminology "pruning" is submitted to be clear.

The Examiner submitted that the recited limitation of "a character sequence expressing the input amino acid sequence" (claim 16) renders the claim indefinite. It is respectfully submitted that paragraph [0118] of the specification recites:

> [0118] FIG. 1 shows a gene information survey apparatus 1 according to an embodiment of the invention. In FIG. 1, the reference numeral 40 denotes input device connected to the gene information survey apparatus 1; the reference numeral 41 denotes an interactive device such as a keyboard and a mouse provided in the input device 40; the reference numeral 42 denotes a display device connected to the gene information survey apparatus 1; the reference numeral 50 denotes an amino acid sequence data base for storing amino acid sequence information expressed by character sequences; and the reference numeral 60 denotes a motif data base for storing motif sequence information expressed by a character sequence. (emphasis added)
>
> [0120] The LCS detection unit 30 determines an LCS (Longest Common Subsequence),

> the length of LCS, and an occurrence position of the LCS between a character sequence expressing an amino acid sequence input from the input device 40 and a character sequence expressing an amino acid sequence taken from the amino acid sequence data base 50 or motif data base 60. The LCS is the longest subsequence among those which commonly occur continuously or intermittently in both character sequences, and the longest common character number is the number of characters constituting the LCS.

Hence, it is respectfully submitted that the terminology "a character sequence expressing the input amino acid sequence" is known to those skilled in the art.

Amended claim 16 recites, and amended claims 23 and 24 in similar fashion, in the preamble: "A method of determining spatially similar portions of a substance comprising amino acids by analyzing three-dimensional structures of the substance, by dividing a molecule of the substance into a plurality of target subsets based on secondary structures and comparing each of the plurality of target subsets of the molecule of the substance to a plurality of probe subsets of a first probe structure, each of the plurality of probe subsets being expressed by three-dimensional coordinates of elements of secondary structures of probe structures, wherein a first subset of the plurality of probe subsets comprises a first point set of an amino acid sequence database or a motif database and each of the plurality of target subsets is expressed by three-dimensional coordinates of elements of the plurality of target subsets of secondary structures of a target structure, wherein a first subset of the plurality of target subsets comprises a second point set of an input amino acid sequence of the target structure, wherein each point of the first point set and the second point set is expressed by three-dimensional coordinates and the coordinates are analyzed to determine correspondence, comprising" (emphasis added). Hence, it is respectfully submitted that there is antecedent basis for the terminology "the input amino acid sequence."

With respect to the double patenting rejection (see also below), Applicants simply request that the Applicants be allowed to address any obviousness-type double patenting issues remaining once the rejection of the claims in the present application are resolved or on allowance of U.S. Patent Application No. 09/910,071. That is, it is premature for Applicants to respond to the double-patenting issue (see MPEP 804 I. B:

> The "provisional" double patenting rejection should continue to be made by the examiner in each application as long as there are conflicting claims in more than one application unless that "provisional" double patenting rejection is the only rejection remaining in at least one of the applications.

Applicants thank the Examiner for his extensive comments in the Advisory Action.

REJECTION UNDER 35 U.S.C. §112:

In the Office Action, at pages 2-8, claims 16, 17, and 23-25 were rejected under 35 U.S.C. §112, second paragraph, for the reasons set forth therein. This rejection is traversed and reconsideration is requested.

Page 4, line 27 through line 23, page 5 of the specification recite:

> When the researcher searches the similar three-dimensional, structure, an r.m.s.d. (root mean square distance) value is used as a scale of the similarity of the three-dimensional structures of the substances. The r.m.s.d. value is a value expressing a square root of a mean square distance between the corresponding elements constituting the substances. Empirically, the substances are thought to be exceedingly similar to each other in the case where the r.m.s.d. value between the substances is not greater than 1 Å. (emphasis added)
>
> For instance, it is assumed that there are substances expressed by a point set $A=\{a_1, a_2, \ldots, a_i, \ldots, a_m\}$ of a target subset, and a point set $B=\{b_1, b_2, \ldots, b_j, \ldots, b_n\}$ of a probe subset, wherein a_i (i=1, 2, . . . , m) and b_j (i=1, 2, . . . , n) are vectors expressing positions of the respective elements in the three-dimensional space. The elements constituting these substances A and B are related to each other, and the substance B is rotated and moved so that the r.m.s.d. value between the corresponding elements is minimized. For example, if a_k is related to b_k (k=1, 2, . . . , n), the r.m.s.d. value is obtained in the following equation (1) wherein U denotes a rotation matrix and W_k denote respective weights:

$$r.m.s.d. = \frac{\left(\sum_{k=1}^{n} \left(w_k (Ub_k - a_k)^2\right)\right)^{\frac{1}{2}}}{n} \quad \ldots(1)$$

(emphasis added).

For clarity, the definition of the r.m.s.d. value has been added to indep claims 16, 23, and 24 in accordance with page 4, line 27 through line 23, page 5 of the s ation.

In addition, the wording of independent claims 16, 23 and 24 has been amended to clarify the source of the subsets (target and probe) and to eliminate redundancy. Antecedent basis has also been corrected. For clarity, the terminology "second structure

The terminologies "wherein each point of the first point set and the second point set is expressed by three-dimensional coordinates and the coordinates are analyzed to determine correspondence" and "wherein the tree structures are generated by successively giving correspondence to an element constituting the sets" have been added to each of the independent claims 16, 23 and 24 to show more clearly that the point sets are expressed by three-dimensional coordinates (see page 53, lines 22-24 of the specification) wherein possible

correspondence is described by a tree structure created by successively giving correspondence to the element constituting the sets (see page 54, lines 13-24 of the specification).

The terminology "attribute" is given its ordinary dictionary definition. For example, in Merriam-Webster Online, attribute is defined as "1: an inherent characteristic; also, an accidental quality 2: an object closely associated with or belonging to a specific person, thing or office ... 3: a word ascribing a quality..." Examples are set forth on page 37, lines 1-10 of the specification. The information encompassed by either a first point set or a second point set is a set of three-dimensional coordinates, and the coordinates are analyzed to determine correspondence (see above). Thus, it is respectfully submitted that the terminology "attribute" and the information encompassed by the first point set and the second point set are clear and definite.

The Examiner submits that the claim fails to delineate any positive steps that result in generating a correspondence. Amended independent claim 16 recites:

> determining whether a correspondence is present between the first point set and the second point set by, for each subset of the plurality of target subsets of secondary structures of the target structure:
>
> generating a first tree structure for the first point set and a second tree structure for the second point set wherein the tree structures are generated by successively giving correspondence to an element constituting the sets;
>
> pruning the second tree structure for the second point set in accordance with a predetermined pruning procedure; and
>
> determining whether the first point set and the second point set have a same attribute, and if the first point set and the second point set have the same attribute, generating a correspondence between the first point set and the second point; and
>
> calculating a root mean square distance (RMSD) value between elements corresponding in the first point set and the second point set to automatically determine a value for a distance between the elements of the first point set and the elements of the second point set, wherein substances expressed by a point set $A=\{a_1, a_2, \ldots, a_i, \ldots, a_m\}$ of a target subset, and a point set $B=\{b_1, b_2, \ldots, b_j, \ldots, b_n\}$ of a probe subset, wherein a_i (i=1, 2, . . . , m) and b_j (i=1, 2, . . . , n) are vectors expressing positions of respective elements in three-dimensional space, elements constituting substances A and B are related to each other, and the substance B is rotated and moved so that the r.m.s.d. value between corresponding elements is minimized in accordance with a following equation (1) wherein U denotes a rotation matrix and W_k denote respective weights:

$$r.m.s.d. = \frac{\left(\sum_{k=1}^{n} \left(w_k (Ub_k - a_k)^2\right)\right)^{\frac{1}{2}}}{n}$$

.....(1);

> determining whether the RMSD is less than or equal to a predetermined threshold value, and where the RMSD is less than or equal to a predetermined threshold value,

generating an optimum correspondence between the first point set of and the second point set;

determining a length of a longest common subsequence (LCS) between a character sequence expressing the input amino acid sequence and a character sequence expressing the amino acid sequence having the optimum correspondence to the input amino acid sequence; and

displaying by a display unit, the longest common subsequence (LCS) between the character sequence expressing the input amino acid sequence and the character sequence expressing the amino acid sequence having the optimum correspondence to the input amino acid sequence.
(emphasis added)

It is respectfully submitted that amended independent claim 16, and similarly, amended independent claims 23 and 24, recite positive steps that result in generating a correspondence (generating a first tree structure for the first point set and a second tree structure for the second point set wherein the tree structures are generated by successively giving correspondence to an element constituting the sets; pruning the second tree structure for the second point set in accordance with a predetermined pruning procedure; and determining whether the first point set and the second point set have a same attribute, and if the first point set and the second point set have the same attribute, generating a correspondence between the first point set and the second point set). As noted above, the terminologies "wherein each point of the first point set and the second point set is expressed by three-dimensional coordinates and the coordinates are analyzed to determine correspondence" and "wherein the tree structures are generated by successively giving correspondence to an element constituting the sets" have been added to each of the independent claims 16, 23 and 24 to show more clearly that the point sets are expressed by three-dimensional coordinates (see page 53, lines 22-24 of the specification), wherein possible correspondence is described by a tree structure created by successively giving correspondence to the element constituting the sets (see page 54, lines 13-24 of the specification). For example, pruning is illustrated in FIG. 18, and is described on page 33, line 10 through page 37, line 25 of the specification. It is respectfully submitted that the process of "pruning" the trees is known to those skilled in the art. Hence, it is respectfully submitted that it is clear how the steps are drawn to generating and pruning a first and a second tree structure and how such is related to generating correspondences between a first and a second point set.

The amendment to include, in independent claims 16, 23 and 24, the terminology "wherein substances expressed by a point set $A=\{a_1, a_2, \ldots, a_i, \ldots, a_m\}$ of a target subset, and a point set $B=\{b_1, b_2, \ldots, b_j, \ldots, b_n\}$ of a probe subset, wherein a_i (i=1, 2, . . . , m) and b_j (i=1, 2, . . . , n) are vectors expressing positions of respective elements in three-dimensional space,

elements constituting substances A and B are related to each other, and the substance B is rotated and moved so that the r.m.s.d. value between corresponding elements is minimized in accordance with a following equation (1) wherein U denotes a rotation matrix and W_k denote respective weights:

$$r.m.s.d. = \frac{\left(\sum_{k=1}^{n} \left(w_k(Ub_k - a_k)^2\right)\right)^{\frac{1}{2}}}{n}$$

.....(1);

is submitted to explain the scope of an "element" and the terminology "point set" is described further above. Hence, it is submitted that the information being relied upon in performing an RBSD calculation is clear. For clarity, the terminology has been amended to recite "calculating a root mean square distance (RMSD) value between elements."

Independent claims 16, 23 and 24 have been amended to recite "predetermined threshold value set by a user." Thus, it is respectfully submitted that the terminology "predetermined threshold value" is now clear and definite.

It is respectfully submitted that on page 16, line 31 through page 17, line 5, the specification recites:

> The LCS detection unit 30 determines an LCS (Longest Common Subsequence), the length of LCS, and an occurrence position of the LCS between a character sequence expressing an amino acid sequence input from the input device 40 and a character sequence expressing an amino acid sequence taken from the amino acid sequence data base 50 or motif data base 60. The LCS is the longest subsequence among those which commonly occur continuously or intermittently in both character sequences, and the longest common character number is the number of characters constituting the LCS. (emphasis added)

Hence, independent claim 16 has been amended to recite: "determining a length of a longest common subsequence (LCS) between a character sequence expressing the input amino acid sequence and a character sequence expressing the amino acid sequence taken from an amino acid sequence data base or a motif data base having the optimum correspondence to the input amino acid sequence." Independent claims 23 and 24 have been amended similarly. Thus, the terminology "a character sequence expressing" is now submitted to be clear.

Hence, amended independent claims 16, 23 and 24 are now submitted to be definite under 35 U.S.C. §112, second paragraph, and to particularly point out and distinctly claim the

subject matter which applicants regard as the invention. Since claims 17 and 25 depend from amended independent claims 16 and 24, respectively, claims 17 and 25 are definite under 35 U.S.C. §112, second paragraph, and particularly point out and distinctly claim the subject matter which applicants regard as the invention for at least the reasons amended independent claims 16 and 24 are definite under 35 U.S.C. §112, second paragraph, and particularly point out and distinctly claim the subject matter which applicants regard as the invention.

DOUBLE PATENTING:

In the Office Action, at pages 8-10, claims 16, 17, and 23 were provisionally rejected on the ground of nonstatutory obviousness-type double patenting as being unpatentable over claim 13 of copending Application No. 09/910,071. This rejection is traversed and reconsideration is requested.

Since U.S. Patent Application No. 09/910,071 has not yet been issued as a patent, and since the all of the claims of the instant application have not yet been indicated as allowable except for the provisional rejection, it is believed that any submission of a Terminal Disclaimer or arguments as to the non-obvious nature of the claims would be premature. MPEP 804(I)(B). As such, it is respectfully requested that the applicants be allowed to address any obviousness-type double patenting issues remaining once the rejection of the claims under 35 U.S.C. § 112 is resolved or on allowance of U.S. Patent Application No. 09/910,071.

EXAMINER'S RESPONSE TO ARGUMENTS:

In the Office Action, at pages 10-18, the Examiner responded to Applicants' arguments filed 9/11/2006.

The Examiner submitted that the terminology "R.M.S.D." is still unclear. Independent claims 16, 23 and 24 have been amended to include the definition of R.M.S.D., and for clarity, the terminology "root mean square distance (RMSD)" has been amended to recite "root mean square distance (RMSD) value." Dependent claims 17 and 25 are clear for at least the reasons amended independent claims 16 and 24 are clear. Hence, the terminology R.M.S.D. is now submitted to be clear.

The Examiner is concerned with the terminology "a first probe structure expressed by the three-dimensional coordinates of elements belonging to a first probe subset of a plurality of subsets of a secondary structure of probe structures, the first subset comprising a first point set of an amino acid sequence or a motif database." Independent claims 16, 23 and 24 have been amended to clarify the subset terminology by referring to the subsets of the target as the target

subsets and the subsets of the probe as the probe subsets. Also, independent claims 16, 23 and 24 have been amended to recite "wherein each point of the first point set and the second point set is expressed by three-dimensional coordinates and the coordinates are analyzed to determine correspondence." Dependent claims 17 and 25 are clear for at least the reasons amended independent claims 16 and 24 are clear. Hence, the terminology cited above is now submitted to be clear.

The Examiner is concerned with the language "a target structure expressed by three-dimensional coordinates of elements belonging to a second subset of a plurality of subsets of secondary structures of the target structure, the second subset comprising a second point set of an input amino acid sequence of the target structure." Independent claims 16, 23 and 24 have been amended to clarify the "subset" language" and to recite "wherein each point of the first point set and the second point set is expressed by three-dimensional coordinates and the coordinates are analyzed to determine correspondence." Independent claims 16, 23 and 24 have been further amended to include the terminology "wherein substances expressed by a point set $A=\{a_1, a_2, \ldots, a_i, \ldots, a_m\}$ of a target subset and a point set $B=\{b_1, b_2, \ldots, b_j, \ldots, b_n\}$ of a probe subset, wherein a_i (i=1, 2, . . . , m) and b_j (i=1, 2, . . . , n) are vectors expressing positions of respective elements in three-dimensional space, elements constituting substances A and B are related to each other, and the substance B is rotated and moved so that the r.m.s.d. value between corresponding elements is minimized in accordance with a following equation (1) wherein U denotes a rotation matrix and W_k denote respective weights." Dependent claims 17 and 25 are clear for at least the reasons amended independent claims 16 and 24 are clear. Hence, said language is now submitted to be clear.

The Examiner is concerned with the terminology "dividing the second target structure into a plurality of second subsets based on secondary structures of the three-dimensional coordinates of the target structure." The "subset" language has been amended for clarity. It is respectfully submitted that the amendment to add, to independent claims 16, 23, and 24, the terminology "wherein substances expressed by a point set $A=\{a_1, a_2, \ldots, a_i, \ldots, a_m\}$ of a target subset, and a point set $B=\{b_1, b_2, \ldots, b_j, \ldots, b_n\}$ of a probe subset, wherein a_i (i=1, 2, . . . , m) and b_j (i=1, 2, . . . , n) are vectors expressing positions of respective elements in three-dimensional space, elements constituting substances A and B are related to each other, and the substance B is rotated and moved so that the r.m.s.d. value between corresponding elements is minimized in accordance with a following equation (1) wherein U denotes a rotation matrix and W_k denote respective weights" clarifies how the division of the target structure into a plurality of

subsets results in generation of a distinct set of subset structures. Dependent claims 17 and 25 are clear for at least the reasons amended independent claims 16 and 24 are clear.

The Examiner is concerned with a step drawn to determining whether a correspondence is present between the first point set and the second point set by (i) generating a first tree structure for the first point set and a second tree structure for the second point set, (ii) pruning the second tree structure for the second point set, (iii) determining whether the first point set and the second point set have a same attribute, and (iv) if the first point set and the second point set have a same attribute, generating a correspondence between the first point set and the second point set. Claims 16, 23 and 24 have been amended to clarify the operations of the present invention (see above). The terminology "attribute" has its common dictionary definition, and thus is submitted to be clear. The scope of the terminology "attribute" is clear from the specification (see above). Thus, amended independent claims 16, 23 and 24 are submitted to be clear with respect to the above-cited Examiner's concern. Dependent claims 17 and 25 are clear for at least the reasons amended independent claims 16 and 24 are clear.

The Examiner is concerned with the terminology "calculating a root mean square distance (RMSD) between elements corresponding in the first point set of the probe structure and the second point set of the plurality of second subsets of the target structure to automatically determine a distance between the elements of the first point set and the elements of the second point set." This terminology has been amended for clarity (see above). For example, the terminology "root mean square distance (RMSD)" has been amended to recite "root mean square distance (RMSD) value" and "to automatically determine a distance" has been amended to recite "to automatically determine a value for a distance." The point sets have been described by adding the terminology "wherein each point of the first point set and the second point set is expressed by three-dimensional coordinates and the coordinates are analyzed to determine correspondence." The "element" terminology has been clarified by adding the terminology "wherein substances expressed by a point set $A=\{a_1, a_2, \ldots, a_i, \ldots, a_m\}$ of a target subset, and a point set $B=\{b_1, b_2, \ldots, b_j, \ldots, b_n\}$ of a probe subset, wherein a_i (i=1, 2, . . . , m) and b_j (i=1, 2, . . . , n) are vectors expressing positions of respective elements in three-dimensional space, elements constituting substances A and B are related to each other." Hence, said terminology is now believed to be clear in amended independent claims 16, 23 and 24. Dependent claims 17 and 25 are clear for at least the reasons amended independent claims 16 and 24 are clear.

The Examiner is concerned with the terminology "a predetermined threshold value." Said terminology has been amended to recite "a predetermined threshold value set by a user," and is

now submitted to be clear in amended independent claims 16, 23 and 24. Dependent claims 17 and 25 are clear for at least the reasons amended independent claims 16 and 24 are clear.

The Examiner is concerned with the terminology "a character sequence expressing the input amino acid sequence" and "a character sequence expressing the amino acid sequence." In independent claims 16, 23 and 24, said terminology has been amended for clarity to recite: "determining a length of a longest common subsequence (LCS) between a character sequence expressing the input amino acid sequence and a character sequence expressing the amino acid sequence taken from an amino acid sequence data base or a motif data base having the optimum correspondence to the input amino acid sequence" based on page 16, line 31 through page 17, line 2 of the specification. Dependent claims 17 and 25 are clear for at least the reasons amended independent claims 16 and 24 are clear.

Hence, it is respectfully submitted that the Examiner's concerns have been overcome by the present amendments.

CONCLUSION:

In accordance with the foregoing, it is respectfully submitted that all outstanding objections and rejections have been overcome and/or rendered moot, and further, that all pending claims patentably distinguish over the prior art. Thus, there being no further outstanding objections or rejections, the application is submitted as being in condition for allowance which action is earnestly solicited. At a minimum, this Amendment should be entered at least for purposes of Appeal as it either clarifies and/or narrows the issues for consideration by the Board.

If the Examiner has any remaining issues to be addressed, it is believed that prosecution can be expedited and possibly concluded by the Examiner contacting the undersigned attorney for a telephone interview to discuss any such remaining issues.

If there are any underpayments or overpayments of fees associated with the filing of this Amendment, please charge and/or credit the same to our Deposit Account No. 19-3935.

Respectfully submitted,

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